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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:36:52 ; Search time 11 Seconds
(without alignments)
41.789 Million cell updates/sec

Title: US-10-646-770-2
Perfect score: 96
Sequence: 1 MCCTKSLLLAALMSVLLHL.....PKQTVWYIVRLLSKKVKNM 96

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 26661 seqs, 4788334 residues

Word size : 6

Total number of hits satisfying chosen parameters: 33

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	7.3	265	6 US-10-793-626-2500	Sequence 2500, Ap
2	7	7.3	345	6 US-10-467-657-7598	Sequence 7598, Ap
3	7	7.3	419	6 US-10-467-657-8064	Sequence 8064, Ap
4	7	7.3	488	6 US-10-821-234-1000	Sequence 1000, Ap
5	7	7.3	697	7 US-11-082-389-362	Sequence 362, App
6	6	6.2	87	6 US-10-467-657-8698	Sequence 8698, Ap
7	6	6.2	140	6 US-10-467-657-7270	Sequence 7270, Ap
8	6	6.2	177	6 US-10-980-388-94	Sequence 94, Appl
9	6	6.2	182	7 US-11-074-176-246	Sequence 246, App
10	6	6.2	229	6 US-10-131-826A-410	Sequence 410, App
11	6	6.2	229	6 US-10-467-657-5756	Sequence 5756, Ap
12	6	6.2	243	6 US-10-467-657-3362	Sequence 3362, Ap
13	6	6.2	276	6 US-10-467-657-6	Sequence 6, Appli
14	6	6.2	276	6 US-10-467-657-4158	Sequence 4158, Ap
15	6	6.2	281	6 US-10-131-826A-54	Sequence 54, Appl
16	6	6.2	323	6 US-10-821-234-981	Sequence 981, App
17	6	6.2	337	6 US-10-980-388-115	Sequence 115, App
18	6	6.2	348	6 US-10-467-657-8200	Sequence 8200, Ap
19	6	6.2	356	6 US-10-467-657-4740	Sequence 4740, Ap
20	6	6.2	358	6 US-10-793-626-2136	Sequence 2136, Ap
21	6	6.2	358	6 US-10-980-388-96	Sequence 96, Appl
22	6	6.2	365	6 US-10-793-626-470	Sequence 470, App
23	6	6.2	365	7 US-11-108-528-56	Sequence 56, Appl
24	6	6.2	365	7 US-11-108-528-58	Sequence 58, Appl
25	6	6.2	389	6 US-10-980-388-116	Sequence 116, App

26	6	6.2	529	6 US-10-821-234-1520	Sequence 1520, Ap
27	6	6.2	658	6 US-10-821-234-921	Sequence 921, App
28	6	6.2	676	6 US-10-510-947-1	Sequence 1, Appli
29	6	6.2	825	7 US-11-074-176-20	Sequence 20, Appl
30	6	6.2	881	7 US-11-191-374-12	Sequence 12, Appl
31	6	6.2	881	7 US-11-191-375-12	Sequence 12, Appl
32	6	6.2	961	6 US-10-831-997-4	Sequence 4, Appli
33	6	6.2	3433	6 US-10-714-781A-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2500

Query Match 7.3%; Score 7; DB 6; Length 265;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 ROLANEG 57
|||||||
Db 205 ROLANEG 211

RESULT 2
US-10-467-657-7598
; Sequence 7598, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7598
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7598

Query Match 7.3%; Score 7; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAALM 13
| | | | |
Db 159 LLLAALM 165

RESULT 3

US-10-467-657-8064
; Sequence 8064, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8064
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8064

Query Match 7.3%; Score 7; DB 6; Length 419;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLLAAL 12
| | | | |
Db 78 SLLLAAL 84

RESULT 4

US-10-821-234-1000
; Sequence 1000, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1000
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1000

Query Match 7.3%; Score 7; DB 6; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLLAAL 12
| | | | |
Db 31 SLLLAAL 37

RESULT 5

US-11-082-389-362
; Sequence 362, Application US/11082389

; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 362
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-362

Query Match 7.3%; Score 7; DB 7; Length 697;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LAALMSV 15
| | | | |
Db 322 LAALMSV 328

RESULT 6

US-10-467-657-8698
; Sequence 8698, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8698
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8698

Query Match 6.2%; Score 6; DB 6; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LLLAA 11
| | | | |
Db 76 LLLAA 81

RESULT 7
US-10-467-657-7270
; Sequence 7270, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7270
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7270

Query Match 6.2%; Score 6; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAAL 12
| | | | |
Db 7 LLLAAL 12

RESULT 8
US-10-980-388-94
; Sequence 94, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880

; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-94

Query Match 6.2%; Score 6; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAAL 12
| | | | |
Db 119 LLLAAL 124

RESULT 9
US-11-074-176-246
; Sequence 246, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-246

Query Match 6.2%; Score 6; DB 7; Length 182;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 AASNFD 31
| | | | |
Db 146 AASNFD 151

RESULT 10
US-10-131-826A-410
; Sequence 410, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-410
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Query Match      6.2%; Score 6; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 LLLAAL 12
        |||||
Db      12 LLLAAL 17
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```
RESULT 11
US-10-467-657-5756
; Sequence 5756, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 1.04
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5756
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5756
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Query Match      6.2%; Score 6; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      84 YIVRL 89
        |||||
Db      220 YIVRL 225
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RESULT 12
US-10-467-657-3362
; Sequence 3362, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3362
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3362
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Query Match      6.2%; Score 6; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      6 SLLLA 11
        |||||
Db      35 SLLLA 40
```

```
RESULT 13
US-10-467-657-6
; Sequence 6, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6
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Query Match      6.2%; Score 6; DB 6; Length 276;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 LLLAAL 12
        |||||
```


Db 26 LLLAAL 31

RESULT 14

US-10-467-657-4158

; Sequence 4158, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; PRIOR FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 4158

; LENGTH: 276

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-4158

Query Match

Best Local Similarity 6.2%; Score 6; DB 6; Length 276;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAAL 12

Db 26 LLLAAL 31

RESULT 15

US-10-131-826A-54

; Sequence 54, Application US/10131826A

; Publication No. US20050245730A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C128

; CURRENT APPLICATION NUMBER: US/10/131,826A

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 54

; LENGTH: 281

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-131-826A-54

Query Match

Best Local Similarity 6.2%; Score 6; DB 6; Length 281;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLLA 11

Db 5 SLLLA 10

RESULT 16

US-10-821-234-981

; Sequence 981, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt_SEQ_genes Version 1.0

; SEQ ID NO 981

; LENGTH: 323

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-981

Query Match

Best Local Similarity 6.2%; Score 6; DB 6; Length 323;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 IVGFTR 51

Db 214 IVGFTR 219

RESULT 17

US-10-980-388-115

; Sequence 115, Application US/10980388

; Publication No. US20050255490A1

; GENERAL INFORMATION:

; APPLICANT: Vogeli, Gabriel

; APPLICANT: Parodi, Luis A.

; APPLICANT: Hiebsch, Ronald R.

; APPLICANT: Lind, Peter

; APPLICANT: Kaytes, Paul S.

; APPLICANT: Ruff, Valerie

; APPLICANT: Huff, Rita M.

; APPLICANT: Wood, Linda S.

; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appli

```

; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-115

Query Match      6.2%; Score 6; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 LLLAAL 12
      |||||
Db      123 LLLAAL 128

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RESULT 18
US-10-467-657-8200
; Sequence 8200, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8200
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8200

Query Match      6.2%; Score 6; DB 6; Length 348;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      47 VGFTRQ 52
      |||||
Db      341 VGFTRQ 346

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RESULT 19
US-10-467-657-4740
; Sequence 4740, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4740
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4740

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Query Match      6.2%; Score 6; DB 6; Length 356;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 LLLAAL 12
      |||||
Db      236 LLLAAL 241

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```

RESULT 20
US-10-793-626-2136
; Sequence 2136, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2136
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2136

```

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Query Match      6.2%; Score 6; DB 6; Length 358;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      6 SLLLA 11
      |||||
Db      47 SLLLA 52

```

```

RESULT 21
US-10-980-388-96
; Sequence 96, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.

```


Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAAL 12
 |||||
Db 19 LLLAAL 24

RESULT 25
US-10-980-388-116
; Sequence 116, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-116

Query Match 6.2%; Score 6; DB 6; Length 389;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAAL 12
 |||||
Db 58 LLLAAL 63

Search completed: December 3, 2005, 14:45:49
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:33:51 ; Search time 37 Seconds
(without alignments)
249.643 Million cell updates/sec

Title: US-10-646-770-2
Perfect score: 96
Sequence: 1 MCCTKSLLLAALMSVLLHL.....PKQTVWKYIVRLLSKVKVNM 96

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 283416 seqs, 96216763 residues

Word size : 6
Total number of hits satisfying chosen parameters: 581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	8.3	345	2 F83712	ribonucleoside-dip
2	7	7.3	63	2 E82584	hypothetical prote
3	7	7.3	153	2 A55889	hypothetical 16.2K
4	7	7.3	153	2 D86131	hypothetical prote
5	7	7.3	153	2 G91289	hypothetical prote
6	7	7.3	157	2 C69470	dCMP deaminase hom
7	7	7.3	160	2 B95973	hypothetical expor
8	7	7.3	201	2 T43151	hypothetical prote
9	7	7.3	212	2 F84481	Mutator-like trans
10	7	7.3	238	2 I62385	outer membrane pro
11	7	7.3	240	2 I62394	outer membrane pro
12	7	7.3	241	2 I62387	outer membrane pro
13	7	7.3	241	2 I62391	outer membrane pro
14	7	7.3	243	2 I84531	outer membrane pro
15	7	7.3	243	2 I62388	outer membrane pro
16	7	7.3	335	2 A70128	conserved hypothet
17	7	7.3	346	1 NMECA	outer membrane pro
18	7	7.3	346	2 A90759	outer membrane pro
19	7	7.3	346	2 G85622	outer membrane pro
20	7	7.3	350	2 S07222	outer membrane pro
21	7	7.3	350	2 S51494	arabinogalactan en
22	7	7.3	351	1 NMEBAD	outer membrane pro
23	7	7.3	354	2 E83291	probable secretion
24	7	7.3	356	2 JC6558	outer membrane pro
25	7	7.3	359	2 JC7280	cytokine receptor-
26	7	7.3	366	2 G82069	conserved hypothet
27	7	7.3	407	2 F75158	hypothetical prote
28	7	7.3	419	2 G82009	SUN homolog NMA016
29	7	7.3	419	2 B81236	16S RNA methyltran

30	7	7.3	422	2 T33186	hypothetical prote
31	7	7.3	450	2 E96738	hypothetical prote
32	7	7.3	463	2 S66504	dipeptidyl-peptida
33	7	7.3	469	2 D81017	chloride channel p
34	7	7.3	524	2 JC8017	beta-galactoside a
35	7	7.3	540	2 B70709	hypothetical prote
36	7	7.3	571	2 T36317	two-component sens
37	7	7.3	603	2 S53301	H+-exporting ATPas
38	7	7.3	769	1 WZBE54	gene 54 protein -
39	7	7.3	825	2 I46078	endothelin convert
40	7	7.3	1280	1 DVHU1	multidrug resistan
41	7	7.3	1398	2 T20434	hypothetical prote
42	7	7.3	1417	2 H83132	probable sensor/re
43	7	7.3	2352	2 C83229	probable non-ribos
44	6	6.2	23	2 A31944	cytochrome P450NMA
45	6	6.2	48	2 B69606	spore coat protein
46	6	6.2	56	2 A24823	interleukin-2 homo
47	6	6.2	63	2 C91290	hypothetical prote
48	6	6.2	65	2 D72152	B20L protein - var
49	6	6.2	66	2 H98064	hypothetical prote
50	6	6.2	83	2 H69183	hypothetical prote
51	6	6.2	89	1 VDBPL	kil protein - phag
52	6	6.2	89	2 A99776	Kil protein [impor
53	6	6.2	89	2 C85848	hypothetical prote
54	6	6.2	89	2 F91003	Kil protein [impor
55	6	6.2	89	2 B85638	probable Kil prote
56	6	6.2	89	2 C84939	flagellar biosynth
57	6	6.2	89	2 AI0221	flagellar biosynth
58	6	6.2	90	2 B35532	proline-rich prote
59	6	6.2	90	2 PC2137	hypothetical 90 pr
60	6	6.2	90	2 PC2136	Lim1 protein - tru
61	6	6.2	94	2 H70654	hypothetical prote
62	6	6.2	95	2 D95198	conserved domain p
63	6	6.2	97	1 GECH	osteocalcin precu
64	6	6.2	101	2 F83951	hypothetical prote
65	6	6.2	107	2 H75397	hypothetical prote
66	6	6.2	108	2 AB0636	conserved hypothet
67	6	6.2	108	2 JC6041	agfC protein precu
68	6	6.2	110	2 S70789	cagC protein precu
69	6	6.2	110	2 A85666	probable curli pro
70	6	6.2	110	2 E90806	probable curli pro
71	6	6.2	111	2 T37114	hypothetical prote
72	6	6.2	111	2 AC0733	probable exported
73	6	6.2	115	2 F75284	hypothetical prote
74	6	6.2	117	2 JC2210	thypothetical 12.6
75	6	6.2	120	2 T41017	hypothetical HXC-2
76	6	6.2	122	2 A72755	hypothetical prote
77	6	6.2	123	1 RHBOG	galanin precursor
78	6	6.2	123	1 RHUN	galanin precursor
79	6	6.2	127	2 A25864	calcitonin gene-re
80	6	6.2	128	1 TCHUR	calcitonin gene-re
81	6	6.2	128	1 A57321	E48 antigen precu
82	6	6.2	131	2 D83173	hypothetical prote
83	6	6.2	132	2 T11239	hypothetical prote
84	6	6.2	134	2 A44173	calcitonin gene-re
85	6	6.2	135	2 F64034	hypothetical prote
86	6	6.2	135	2 F83611	hypothetical prote
87	6	6.2	137	2 A35934	calcitonin precurs
88	6	6.2	138	2 A33334	Ig heavy chain pre
89	6	6.2	140	2 H81197	probable secreted
90	6	6.2	141	1 TCHU	calcitonin precurs
91	6	6.2	141	2 A41716	calcitonin precurs
92	6	6.2	142	2 AC0928	probable regulator
93	6	6.2	143	1 TCSH	calcitonin precurs
94	6	6.2	146	1 PSRT	phospholipase A2 (
95	6	6.2	147	2 F71089	Ni,Fe-Hydrogenase
96	6	6.2	152	2 AB2888	conserved hypothet
97	6	6.2	152	2 G97663	hypothetical prote
98	6	6.2	154	2 S36527	E6 protein - human
99	6	6.2	154	2 A95177	acetyltransferase,
100	6	6.2	154	2 C98043	hypothetical prote
101	6	6.2	157	2 T34552	hypothetical prote
102	6	6.2	158	2 C96005	conserved hypothet

103 6 6.2 160 2 S54747 cyclL protein - Bra
104 6 6.2 160 2 T36282 probable tryptopha
105 6 6.2 166 2 B83315 NADH dehydrogenase
106 6 6.2 167 2 AE0440 molybdenum cofacto
107 6 6.2 168 2 E75257 secreted protein H
108 6 6.2 172 2 G82987 hypothetical prote
109 6 6.2 172 2 A03857 hypothetical prote
110 6 6.2 174 2 C72737 probable PTS syste
111 6 6.2 180 2 F71284 L-fucose-phospha
112 6 6.2 181 1 A64477 conserved hypothet
113 6 6.2 183 2 D83069 ribosomal protein
114 6 6.2 184 1 S47020 hypothetical prote
115 6 6.2 185 2 F64459 hypothetical prote
116 6 6.2 187 2 C90539 calcium-binding pr
117 6 6.2 192 1 KLSBS phosphoenolpyruvat
118 6 6.2 192 2 T09847 glutathione S-tran
119 6 6.2 195 2 H87388 sodium-dependent p
120 6 6.2 202 2 AC3318 hypothetical prote
121 6 6.2 203 2 AF1199 hypothetical prote
122 6 6.2 203 2 AD1557 GTP cyclohydrolase
123 6 6.2 204 2 T39940 probable two-compo
124 6 6.2 204 2 T29444 probable lipoprote
125 6 6.2 207 2 AI0245 probable membrane
126 6 6.2 208 2 AC0465 ATP-dependent Clp
127 6 6.2 210 2 F87492 clpp (AF218420) [i
128 6 6.2 210 2 E97512 ATP-dependent Clp
129 6 6.2 211 2 AF0011 probable exported
130 6 6.2 211 2 T35272 hypothetical prote
131 6 6.2 211 2 T35272 conserved hypothet
132 6 6.2 212 2 E82125 conserved hypothet
133 6 6.2 213 2 G75303 glutathione transf
134 6 6.2 218 2 A39375 glutamine ABC tran
135 6 6.2 218 2 F69633 conserved hypothet
136 6 6.2 218 2 T40365 conserved hypothet
137 6 6.2 221 2 E64400 hypothetical prote
138 6 6.2 222 2 C75250 probable oxidoredu
139 6 6.2 222 2 T36115 uroporphyrinogen I
140 6 6.2 222 2 C89950 probable integral
141 6 6.2 224 2 T34686 MADS box protein T
142 6 6.2 227 2 S23730 probable RING zinc
143 6 6.2 227 2 T02413 probable amino aci
144 6 6.2 228 2 C95931 hypothetical prote
145 6 6.2 228 2 T22266 germin-like protei
146 6 6.2 229 2 T05956 conserved hypothet
147 6 6.2 229 2 D81867 conserved hypothet
148 6 6.2 229 2 H81073 proline-rich prote
149 6 6.2 230 1 FUSY3 probable methyltra
150 6 6.2 233 2 T35286 hypothetical prote
151 6 6.2 236 2 T36188 25K outer-membrane
152 6 6.2 236 2 AI3377 permatin homolog P
153 6 6.2 237 2 T05973 hypothetical prote
154 6 6.2 237 2 B71424 HNF-3/fork head tr
155 6 6.2 237 2 A47368 Ki nuclear autoant
156 6 6.2 239 2 B60537 tRNA/rRNA methyltr
157 6 6.2 240 2 A97826 hypothetical prote
158 6 6.2 240 2 E64897 hypothetical prote
159 6 6.2 240 2 F90885 hypothetical prote
160 6 6.2 240 2 A85733 hypothetical prote
161 6 6.2 241 2 T48006 (R) -2-hydroxygluta
162 6 6.2 243 2 D64300 hypothetical cytos
163 6 6.2 243 2 AE3390 conserved hypothet
164 6 6.2 248 2 AD2687 BH0857 hypothetica
165 6 6.2 248 2 H97468 hypothetical prote
166 6 6.2 248 2 G83238 hypothetical-like pr
167 6 6.2 249 2 T48603 MADS box protein -
168 6 6.2 250 2 T07902 MADS box protein h
169 6 6.2 250 2 T07100 (3R) -hydroxymyrist
170 6 6.2 251 2 D75439 DitB protein [impo
171 6 6.2 253 2 T50942 probable lipoprote
172 6 6.2 253 2 AI0613 hypothetical prote
173 6 6.2 255 2 T28121 proline-rich prote
174 6 6.2 256 2 A29324 molybdate ABC tran
175 6 6.2 256 2 AI1204

176 6 6.2 259 2 AE3108 outer membrane lip
177 6 6.2 259 2 G98178 probable periplasm
178 6 6.2 261 2 A83281 periplasmic histid
179 6 6.2 265 2 S31070 rpcE protein - Syn
180 6 6.2 265 2 H75416 conserved hypothet
181 6 6.2 266 1 A35802 15-hydroxyprostagl
182 6 6.2 267 2 A60537 Ki nuclear autoant
183 6 6.2 267 2 E87269 exopolysaccharide
184 6 6.2 267 2 T06613 hypothetical prote
185 6 6.2 269 2 D64668 hypothetical prote
186 6 6.2 269 2 E72693 hypothetical prote
187 6 6.2 269 2 AH2268 hypothetical prote
188 6 6.2 271 2 G89809 SAM-dependent meth
189 6 6.2 272 2 E96989 membrane protein n
190 6 6.2 273 2 AI3630 monofunctional bio
191 6 6.2 273 2 F82646 nosy protein [impo
192 6 6.2 275 2 T44663 unknown protein [i
193 6 6.2 275 2 A86388 hypothetical prote
194 6 6.2 276 2 I39705 endopeptidase Clp
195 6 6.2 277 1 S68421 Outer membrane 30K
196 6 6.2 277 2 JN0751 probable exported
197 6 6.2 277 2 AE0661 phytoene synthetas
198 6 6.2 277 2 G90469 conserved hypothet
199 6 6.2 278 2 E81658 hypothetical prote
200 6 6.2 278 2 A71498 pantoate beta-alan
201 6 6.2 283 2 F90066 branched-chain ami
202 6 6.2 285 2 E75539 hypothetical prote
203 6 6.2 288 2 T41112 xap-5-like protein
204 6 6.2 288 2 T40828 conserved hypothet
205 6 6.2 291 2 E82226 hypothetical prote
206 6 6.2 294 2 D83108 hypothetical prote
207 6 6.2 295 2 E75466 ribosomal protein
208 6 6.2 296 2 E71717 hypothetical prote
209 6 6.2 296 2 T20005 lytic enzyme lysA
210 6 6.2 297 2 S38477 urea/short-chain a
211 6 6.2 300 2 F75586 conserved hypothet
212 6 6.2 300 2 H90152 probable binding p
213 6 6.2 302 2 H83478 hypothetical prote
214 6 6.2 303 1 H71246 sugar ABC transpor
215 6 6.2 303 2 AE3520 N-acetylneuraminat
216 6 6.2 305 2 B95154 NADH2 dehydrogenas
217 6 6.2 306 2 T07684 transcription regu
218 6 6.2 306 2 F70389 probable cell divi
219 6 6.2 311 2 C84807 conserved hypothet
220 6 6.2 311 2 T09586 succinate dehydrog
221 6 6.2 313 2 D69336 NADH dehydrogenase
222 6 6.2 314 1 T50537 dual specificity p
223 6 6.2 314 2 H84221 ferrichrome ABC tr
224 6 6.2 315 1 B69812 probable ABC trans
225 6 6.2 315 2 A95275 highly charged pro
226 6 6.2 315 2 I37273 hypothetical prote
227 6 6.2 316 2 T23640 NADH2 dehydrogenas
228 6 6.2 316 2 S68157 probable permease
229 6 6.2 317 2 B83039 hypothetical prote
230 6 6.2 317 2 B86183 envelope glycoprot
231 6 6.2 318 2 S23155 hypothetical prote
232 6 6.2 319 2 T49458 conserved hypothet
233 6 6.2 321 2 E81668 hypothetical prote
234 6 6.2 321 2 A71510 sugar ABC transpor
235 6 6.2 321 2 C83940 suhR protein - Rhi
236 6 6.2 323 2 A44504 hypothetical prote
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242 6 6.2 330 2 G88115 sensor histidine k
243 6 6.2 331 2 H95044 probable transcrip
244 6 6.2 331 2 H95876 histidine kinase (
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246 6 6.2 333 2 B90172 hypothetical prote
247 6 6.2 333 2 G71801

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 278 hypothetical prote 379 2 S74601 6 6.2
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3-phosphoshikimate
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 5-enolpyruvylshiki
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 3-phosphoshikimate
 IS605 transposase
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 G protein-coupled
 protein F28J9.8 [i
 hypothetical prote
 aspartate transami
 aspartate transami
 3-phosphoshikimate
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 aspartate transami
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 tolB protein [impo
 allantoinase BH230
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 hypothetical prote
 conserved hypothet
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 enolpyruvylshikima
 tolB protein precu
 McLeod syndrome-as
 probable transmemb
 probable gluconate
 hypothetical prote
 probable MFS trans
 chromosomal replic
 probable transport
 hypothetical prote
 hypothetical prote
 probable cation ef
 probable sodium/so
 probable permease
 probable permease
 hypothetical prote
 acid phosphatase (
 polysaccharide bio
 polysaccharide bio
 multidrug-efflux t
 hypothetical prote
 probable MFS trans
 probable UDP-N-ace
 transporter BME102
 lipopolysaccharide
 major DNA-binding
 amino acid ABC tra
 serine proteinase,
 hypothetical prote
 activating transcr
 NADH2 dehydrogenas
 NADH2 dehydrogenas
 NADH2 dehydrogenas
 NADH2 dehydrogenas
 cytochrome P450 2A
 cytochrome P450 2A
 probable permease
 probable transport
 probable transport
 histidine kinase s
 histidine kinase s
 beta3-glycosyltran
 NADH2 dehydrogenas
 hypothetical prote
 hypothetical prote
 trans-cinnamate 4-
 hypothetical prote
 hydroxymethylgluta

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396	6	6.2	512	2	C42504	C2L protein - vacc	469
397	6	6.2	513	2	T21887	hypothetical prote	470
398	6	6.2	514	2	B69108	phytoene dehydroge	471
399	6	6.2	515	1	A59309	interferon-inducib	472
400	6	6.2	515	2	B84406	TRK potassium upta	473
401	6	6.2	516	1	XUPJVS	3-phosphoshikimate	474
402	6	6.2	516	2	S12744	3-phosphoshikimate	475
403	6	6.2	517	2	A84080	L-arabinose ABC tr	476
404	6	6.2	518	2	S18353	3-phosphoshikimate	477
405	6	6.2	520	1	XUMUVS	3-phosphoshikimate	478
406	6	6.2	520	1	XUTOVS	3-phosphoshikimate	479
407	6	6.2	520	2	H84888	hypothetical prote	480
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410	6	6.2	523	2	D83631	probable sulfate t	483
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412	6	6.2	527	2	T39741	ars binding protei	485
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441	6	6.2	586	2	AH2133	ATP-binding protei	514
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443	6	6.2	588	2	JH0506	adhesion molecule	516
444	6	6.2	588	2	A45254	surface glycoprote	517
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453	6	6.2	615	2	AG0552	protein-export mem	526
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461	6	6.2	672	2	A65024	Hydrogenase-4 comp	534
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467	6	6.2	689	2	E87376	penicillin amidase	540

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743	2	T13673	hypothetical prote
744	2	T35192	probable ABC trans
758	2	T39628	hypothetical prote
775	2	T38929	changed division r
780	2	F96840	hypothetical prote
787	2	S68699	potassium channel
796	2	JC7555	C14orf4 protein -
798	2	AI2053	competence protein
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806	2	T35640	probable sensor ki
807	2	T12177	potassium channel
809	2	A57283	integrin beta chai
815	2	T35970	probable efflux pr
817	2	F83073	probable ATP-depen
829	2	F75415	phosphoenolpyruvat
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835	1	S54216	invasin - Yersinia
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851	2	T41041	probable nucleopor
853	2	A97681	hypothetical prote
853	2	AH2905	conserved hypothet
857	2	JC4169	phosphoenolpyruvat
859	2	T43701	DNA-directed RNA p
862	2	A05028	rpoC protein homol
864	2	T30441	probable capsid-as
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901	2	E70778	probable aceE prot
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911	2	S51441	hypothetical prote
912	2	AI0127	[protein-PII] urid
918	2	C72120	s/t protein kinase
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921	2	S49965	probable membrane
928	2	T01191	RNA-directed DNA p
932	2	S47597	mutL protein homol
936	2	E87115	pyruvate dehydroge
946	2	B87316	TonB-dependent rec
956	2	S40304	phosphoenolpyruvat
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990	2	T43445	hypothetical prote
991	2	S43891	dna exoribonucleas
997	2	T15243	hypothetical prote
999	2	A34307	Ca2+-transporting
999	2	S72267	Ca2+-transporting
1012	2	T42385	alpha-mannosidase
1021	2	AC2202	hypothetical prote
1028	2	AF3286	ATP-dependent DNA
1031	1	A38713	kinesin heavy chai
1044	2	G98332	rnd multidrug effl
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1051	2	D87349	AcrB/AcrD/AcrF fam
1063	2	D83789	hypothetical prote
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569 6 6.2 1956 2 T16416 hypothetical prote
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574 6 6.2 3430 1 GNWVWV genome polypeptid
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ALIGNMENTS

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F83712
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F83712
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <STO>
A;Cross-references: UNIPROT:Q9KFH7; UNIPARC:UPI0000133978; GB:AP001508; GB:BA000004; NID
A;Experimental source: strain C-125
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A;Gene: nrdb
C;Superfamily: ribonucleoside diphosphate reductase beta chain
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DB     107 LAALMSVL 114
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82584
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82584
A;Status: preliminary
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A;Residues: 1-63 <SIM>
A;Cross-references: UNIPROT:Q9PBB3; UNIPARC:UPI00000C2998; GB:AE004035; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tshakho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2231
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DB     36 SLLLAAL 42
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RESULT 3

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N;Alternate names: hypothetical protein f153 (iada 5' region)
C;Species: Escherichia coli
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A55889; S56554; C65247
R;Gary, J.D.; Clarke, S.
J. Biol. Chem. 270, 4076-4087, 1995
A;Title: Purification and characterization of an isoaspartyl dipeptidase from Escherichia
A;Reference number: A55889; MUID:95181377; PMID:7876157
A;Accession: A55889
A;Status: preliminary
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R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8
A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56554
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
```


Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C65247
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Residues: 1-153 <BLAT>
A;Cross-references: UNIPARC:UPI000013B5B0; GB:AE000503; GB:U00096; NID:g1790777; PIDN:AA
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yjiG
C;Superfamily: spore maturation protein, SpmB type

Query Match 7.3%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAALMS 14
| | | | |
Db 72 LLAALMS 78

RESULT 4

D86131
hypothetical protein yjiG [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D86131
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D86131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-153 <STO>
A;Cross-references: UNIPROT:P39378; UNIPARC:UPI000013B5B0; GB:AE005174; NID:g12519340; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yjiG
C;Superfamily: spore maturation protein, SpmB type

Query Match 7.3%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAALMS 14
| | | | |
Db 72 LLAALMS 78

RESULT 5

G91289
hypothetical protein ECs5287 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G91289
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91289
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-153 <HAY>
A;Cross-references: UNIPROT:P39378; UNIPARC:UPI000013B5B0; GB:BA000007; PIDN:BAB38710.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs5287
C;Superfamily: spore maturation protein, SpmB type

Query Match 7.3%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAALMS 14
| | | | |
Db 72 LLAALMS 78

RESULT 6

C69470
dCMP deaminase homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69470
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69470
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-157 <KLE>
A;Cross-references: UNIPROT:O28510; UNIPARC:UPI0000056BDA; GB:AE000981; GB:AE000782; NID
C;Superfamily: Archaeoglobus probable dCMP deaminase

Query Match 7.3%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 LSKKVKN 95
| | | | |
Db 151 LSKKVKN 157

RESULT 7

B95973
hypothetical exported protein [imported] - Sinorhizobium meliloti (strain 1021) magaplas
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95973
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: B95973
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <KUR>
A;Cross-references: UNIPROT:Q92UP5; UNIPARC:UPI00000CB743; GB:AL591985; PIDN:CAC49450.1;
A;Experimental source: strain 1021, megaplasmid pSymb
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB20927
A;Genome: plasmid

Query Match 7.3%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLLAAL 12

Db 10 SLLLAAL 16
|||||
RESULT 8
T43151
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43151
R;Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T43151
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-201 <YOS>
A;Cross-references: UNIPROT:P78893; UNIPARC:UPI000006A723; EMBL:D89244; NID:g1749695; PI
A;Experimental source: strain PR745
Query Match 7.3%; Score 7; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 SVLLLHL 20
Db 189 SVLLLHL 195
|||||
RESULT 9
F84481
Mutator-like transposase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84481
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84481
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <STO>
A;Cross-references: UNIPROT:Q9ZVW8; UNIPARC:UPI00000A832B; GB:AE002093; NID:g3779027; PI
C;Genetics:
A;Gene: At2g07030
A;Map position: 2
Query Match 7.3%; Score 7; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 85 IVRLLSK 91
Db 76 IVRLLSK 82
|||||
RESULT 10
I62385
outer membrane protein ompA - Escherichia vulnexus (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia vulnexus
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62385
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62385
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-238 <RES>
A;Cross-references: UNIPROT:Q99114; UNIPARC:UPI00000B0580; GB:M63348; NID:g146984; PIDN:;
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;98-109/Region: alanine/proline-rich
Query Match 7.3%; Score 7; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 34 LGYTDRI 40
Db 159 LGYTDRI 165
|||||
RESULT 11
I62394
outer membrane protein ompA - Escherichia blattae (ATCC 33430) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia blattae
A;Variety: ATCC 33430
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62394
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62394
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-240 <RES>
A;Cross-references: UNIPROT:Q99124; UNIPARC:UPI000016EC3C; GB:M63345; NID:g147002; PIDN:;
A;Experimental source: ATCC 33430
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;100-111/Region: alanine/proline-rich
Query Match 7.3%; Score 7; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 34 LGYTDRI 40
Db 161 LGYTDRI 167
|||||
RESULT 12
I62387
outer membrane protein A - Escherichia blattae (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia blattae
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62387
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62387
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-241 <RES>
A;Cross-references: UNIPROT:Q99124; UNIPARC:UPI0000130CF2; GB:M63343; NID:g146988; PIDN:;
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;101-112/Region: alanine/proline-rich

Query Match 7.3%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LGYTDRI 40
| | | | |
Db 162 LGYTDRI 168

RESULT 13
I62391
outer membrane protein A - Escherichia blattae (ATCC 33429) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia blattae
A;Variety: ATCC 33429
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62391
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62391
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-241 <RES>
A;Cross-references: UNIPROT:Q99124; UNIPARC:UPI000016EC3B; GB:M63344; NID:G146996; PIDN:
A;Experimental source: ATCC 33429
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;101-112/Region: alanine/proline-rich

Query Match 7.3%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LGYTDRI 40
| | | | |
Db 162 LGYTDRI 168

RESULT 14
I84531
outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia fergusonii
A;Variety: ATCC 35469
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I84531
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I84531
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-243 <RES>
A;Cross-references: UNIPROT:P24747; UNIPARC:UPI000016F6FB; GB:M63351; NID:G146982; PIDN:
A;Experimental source: ATCC 35469
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;103-114/Region: alanine/proline-rich

Query Match 7.3%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LGYTDRI 40
| | | | |
Db 164 LGYTDRI 170

RESULT 15
I62388
outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia fergusonii
A;Variety: ATCC 35472
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62388; I62392
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-243 <RES>
A;Cross-references: UNIPROT:P24747; UNIPARC:UPI0000130CF3; GB:M63352; NID:G146990; PIDN:
A;Experimental source: ATCC 35471
A;Accession: I62392
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-243 <RE2>
A;Cross-references: UNIPARC:UPI0000130CF3; GB:M63353; NID:G146998; PIDN:AAA24240.1; PID:
A;Experimental source: ATCC 35472
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;103-114/Region: alanine/proline-rich

Query Match 7.3%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LGYTDRI 40
| | | | |
Db 164 LGYTDRI 170

RESULT 16
A70128
conserved hypothetical protein BB0225 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Oct-2004
C;Accession: A70128
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: A70128
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-335 <KLE>
A;Cross-references: UNIPROT:O51243; UNIPARC:UPI00000573CB; GB:AE001133; GB:AE000783; NID
A;Experimental source: strain B31
C;Superfamily: tRNA-dihydrouridine synthase

Query Match 7.3%; Score 7; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 RLISKV 93
| | | | |
Db 25 RLISKV 31

RESULT 17
MMECA

Db 258 LGYTDRI 264

RESULT 18
A90759
outer membrane protein 3a ECs1041 [imported] - Escherichia coli (strain O157:H7, substrain C); Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C; Accession: A90759
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands from a patient with hemolytic uremic syndrome
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: A90759
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-346 <HAY>
A; Cross-references: UNIPROT:P02934; UNIPARC:UPI0000130CF0; GB:BA000007; PIDN:BAB34464.1
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: ECs1041
C; Superfamily: outer membrane protein A

	Query Match	7.3%	Score 7;	DB 2;	Length 346;
Best Local Similarity	100.0%;	Pred. No. 44;			
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 34 LGYTDRI 40
|||||
Db 258 LGYTDRI 264

RESULT 19
G85622
outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Accession: G85622
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Miller, L.; Groetbeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: G85622
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-346 <STO>
A; Cross-references: UNIPROT:P02934; UNIPARC:UPI0000130CF0; GB:AE005174; NID:g12514142; P; A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: ompA
C; Superfamily: outer membrane protein A

	Query Match	7.3%	Score 7;	DB 2;	Length 346;
Best Local Similarity	100.0%;	Pred. No. 44;			
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 34 LGYTDRI 40
|||||
Db 258 LGYTDRI 264

RESULT 20
S07222
outer membrane protein ompA precursor - Enterobacter aerogenes
C; Species: Enterobacter aerogenes
C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C; Accession: S07222
R; Braun, G.; Cole, S.T.
Eur. J. Biochem. 137, 495-500, 1983
A; Title: Molecular characterization of the gene coding for major outer membrane protein (OmpA) of Enterobacter aerogenes
A; Reference number: S07222; MUID:84108348; PMID:6363059

JC7280
cytokine receptor-like molecule-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: JC7280
R;Hiroshima, T.; Iwama, A.; Morita, Y.; Nakamura, Y.; Shibuya, A.; Nakauchi, H.
Biochem. Biophys. Res. Commun. 272, 224-229, 2000
A;Title: Molecular cloning and characterization of CRLM-2, a novel type I cytokine recep
A;Reference number: JC7280
A;Contents: Embryo
A;Accession: JC7280
A;Molecule type: mRNA
A;Residues: 1-359 <HIR>
A;Cross-references: UNIPARC:UPI000017C648; DDBJ:AB039945
C;Genetics:
A;Gene: crlm-2
C;Keywords: cytokine; embryo; receptor; signal transduction; transmembrane protein

Query Match 7.3%; Score 7; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLLAAL 12
|||
Db 247 SLLLAAL 253

Search completed: December 3, 2005, 14:44:49
Job time : 56 secs

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